Saccharomyces Genome Database Integrates Transcriptional Regulation Data

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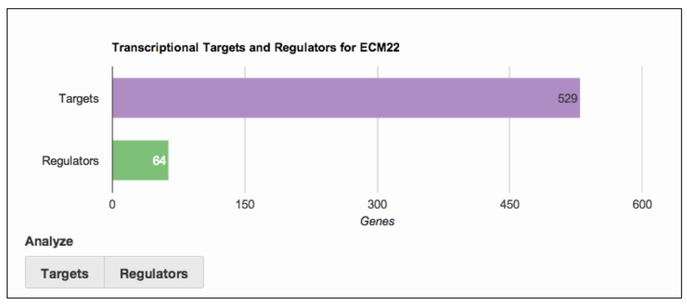
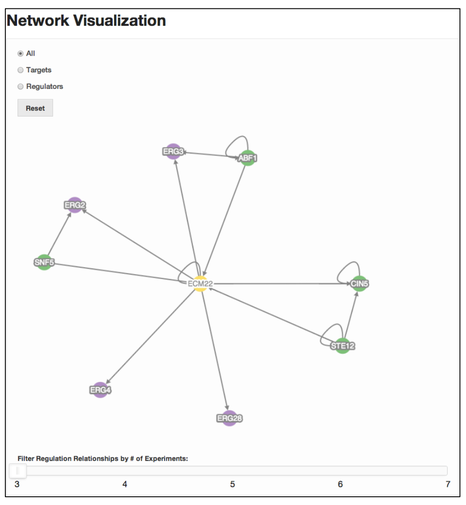
Transcriptional regulation has been heavily studied in the yeast *Saccharomyces cerevisiae*, and huge amounts of data have been generated from both small- and large-scale experiments. To help researchers access and understand these data, the *Saccharomyces* Genome Database (SGD; http://www.yeastgenome.org) has compiled all published transcriptional regulator-target relationships and presents them on a new tabbed section of the Locus Summary entitled 'Regulation'. Regulatory relationships are curated from the literature at SGD or imported, with permission, from the YEASTRACT database. In addition to the identities of the regulator and target genes, regulation annotations include information such as strain background, direction of regulation, experimental conditions, or confidence scores; each annotation is derived from a published reference. Regulation annotations are presented for each gene in interactive tables that may be sorted, filtered, and downloaded. A graphical visualization of the regulatory network surrounding each gene shows its highest-confidence regulatory relationships and allows the viewer to display the network at different confidence levels. We are adding more information for known transcription factors (TFs), starting with the set of TFs known to bind DNA directly. The Regulation page for each TF has a free-text summary of the regulatory context in which it acts, a table of the protein domains it contains, binding site consensus sequences linked to their genomic locations, and a Gene Ontology enrichment for the regulatory targets of the TF that reveals which processes it regulates. All of the regulation data are available for querying, analysis and download via YeastMine, the InterMine-based data warehouse system in use at SGD.

We thank the YEASTRACT group for permission to display their curated regulatory relationships in SGD. This work is supported by a grant from the US National Human Genome Research Institute (NHGRI) (U41 HG001315).

Overviews of regulation data



View numbers of targets and regulators for a specific gene; analyze or download each set



3 or more supporting annotations

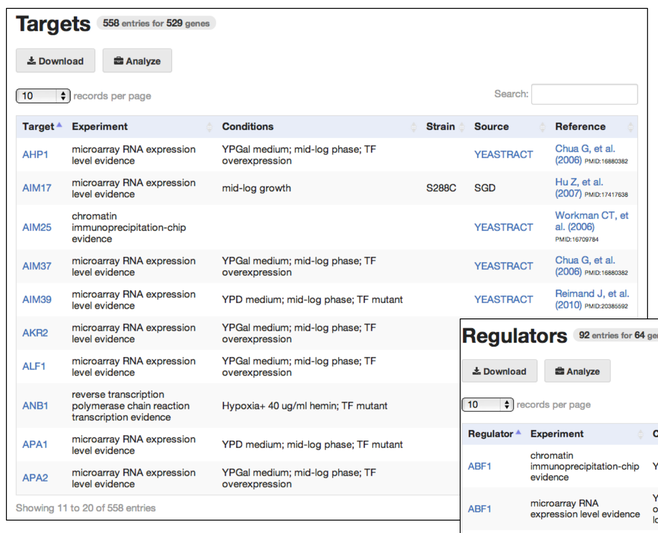
filter

5 or more supporting annotations

View relationship network of targets and regulators; filter by amount of evidence

Detailed regulation annotations

Regulator-target relationships are curated at SGD or imported from YEASTRACT (www.yeastract.com)



Targets 558 entries for 529 genes

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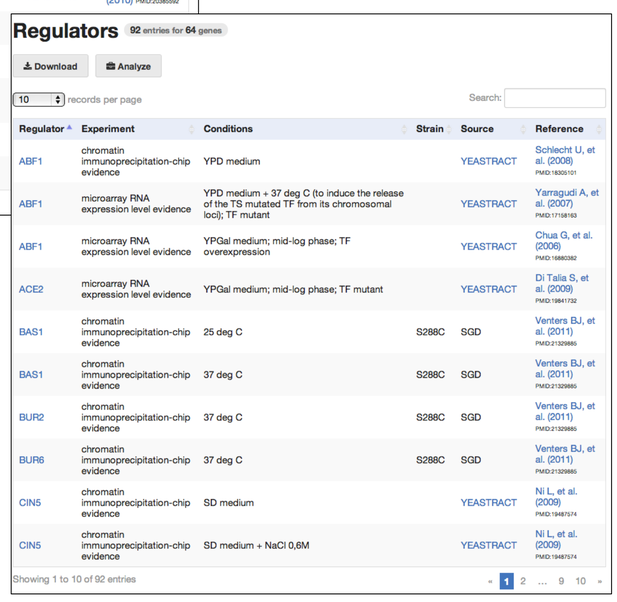
10 records per page — Search:

Target	Experiment	Conditions	Strain	Source	Reference
AHP1	microarray RNA expression level evidence	YPGal medium; mid-log phase; TF overexpression		YEASTRACT	Chua G, et al. (2006) PMID:16880382
AIM17	microarray RNA expression level evidence	mid-log growth	S288C	SGD	Hu Z, et al. (2007) PMID:17417638
AIM25	chromatin immunoprecipitation-chip evidence			YEASTRACT	Workman CT, et al. (2006) PMID:16709784
AIM37	microarray RNA expression level evidence	YPGal medium; mid-log phase; TF overexpression		YEASTRACT	Chua G, et al. (2006) PMID:16880382
AIM39	microarray RNA expression level evidence	YPD medium; mid-log phase; TF mutant		YEASTRACT	Reimand J, et al. (2010) PMID:20385592
AKR2	microarray RNA expression level evidence	YPGal medium; mid-log phase; TF overexpression			
ALF1	microarray RNA expression level evidence	YPGal medium; mid-log phase; TF overexpression			
ANB1	reverse transcription polymerase chain reaction transcription evidence	Hypoxia+ 40 ug/ml hemin; TF mutant			
APA1	microarray RNA expression level evidence	YPD medium; mid-log phase; TF mutant			
APA2	microarray RNA expression level evidence	YPGal medium; mid-log phase; TF overexpression			

Showing 11 to 20 of 558 entries



Regulators 92 entries for 64 genes

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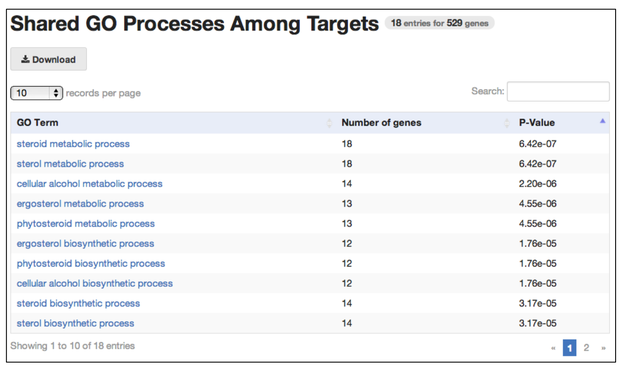
Regulator	Experiment	Conditions	Strain	Source	Reference
ABF1	chromatin immunoprecipitation-chip evidence	YPD medium		YEASTRACT	Schlecht U, et al. (2008) PMID:18305101
ABF1	microarray RNA expression level evidence	YPD medium + 37 deg C (to induce the release of the TS mutated TF from its chromosomal loci); TF mutant		YEASTRACT	Yarragudi A, et al. (2007) PMID:17158163
ABF1	microarray RNA expression level evidence	YPGal medium; mid-log phase; TF overexpression		YEASTRACT	Chua G, et al. (2006) PMID:16880382
ACE2	microarray RNA expression level evidence	YPGal medium; mid-log phase; TF mutant		YEASTRACT	Di Talia S, et al. (2009) PMID:19841732
BAS1	chromatin immunoprecipitation-chip evidence	25 deg C	S288C	SGD	Venters BJ, et al. (2011) PMID:21329885
BAS1	chromatin immunoprecipitation-chip evidence	37 deg C	S288C	SGD	Venters BJ, et al. (2011) PMID:21329885
BUR2	chromatin immunoprecipitation-chip evidence	37 deg C	S288C	SGD	Venters BJ, et al. (2011) PMID:21329885
BUR6	chromatin immunoprecipitation-chip evidence	37 deg C	S288C	SGD	Venters BJ, et al. (2011) PMID:21329885
CIN5	chromatin immunoprecipitation-chip evidence	SD medium		YEASTRACT	Ni L, et al. (2009) PMID:19487574
CIN5	chromatin immunoprecipitation-chip evidence	SD medium + NaCl 0,6M		YEASTRACT	Ni L, et al. (2009) PMID:19487574

Showing 1 to 10 of 92 entries — « 1 2 ... 9 10 »



Shared GO Processes Among Targets 18 entries for 529 genes

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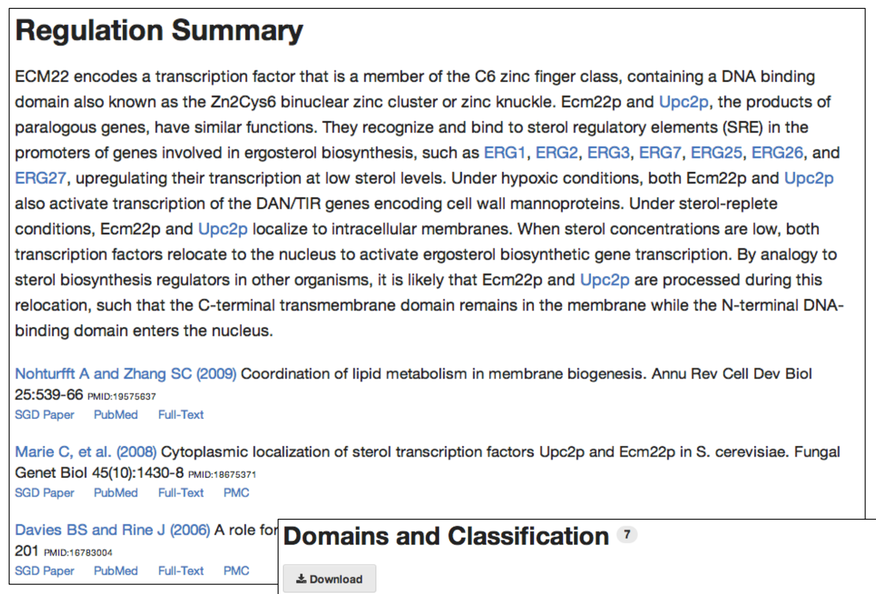
10 records per page — Search:

GO Term	Number of genes	P-Value
steroid metabolic process	18	6.42e-07
sterol metabolic process	18	6.42e-07
cellular alcohol metabolic process	14	2.20e-06
ergosterol metabolic process	13	4.55e-06
phytosteroid metabolic process	13	4.55e-06
ergosterol biosynthetic process	12	1.76e-05
phytosteroid biosynthetic process	12	1.76e-05
cellular alcohol biosynthetic process	12	1.76e-05
steroid biosynthetic process	14	3.17e-05
sterol biosynthetic process	14	3.17e-05

Showing 1 to 10 of 18 entries — « 1 2 »

Tables may be sorted, filtered, downloaded; data also available via YeastMine

Additional information for transcription factors



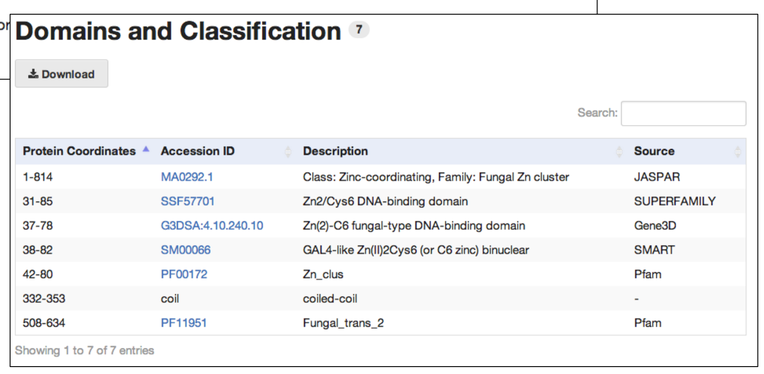
Regulation Summary

ECM22 encodes a transcription factor that is a member of the C6 zinc finger class, containing a DNA binding domain also known as the Zn2Cys6 binuclear zinc cluster or zinc knuckle. Ecm22p and Upc2p, the products of paralogous genes, have similar functions. They recognize and bind to sterol regulatory elements (SRE) in the promoters of genes involved in ergosterol biosynthesis, such as ERG1, ERG2, ERG3, ERG7, ERG25, ERG26, and ERG27, upregulating their transcription at low sterol levels. Under hypoxic conditions, both Ecm22p and Upc2p also activate transcription of the DAN/TIR genes encoding cell wall mannoproteins. Under sterol-replete conditions, Ecm22p and Upc2p localize to intracellular membranes. When sterol concentrations are low, both transcription factors relocate to the nucleus to activate ergosterol biosynthetic gene transcription. By analogy to sterol biosynthesis regulators in other organisms, it is likely that Ecm22p and Upc2p are processed during this relocation, such that the C-terminal transmembrane domain remains in the membrane while the N-terminal DNA-binding domain enters the nucleus.

Nohturfft A and Zhang SC (2009) Coordination of lipid metabolism in membrane biogenesis. Annu Rev Cell Dev Biol 25:539-66 PMID:19575637
SGD Paper PubMed Full-Text

Marie C, et al. (2008) Cytoplasmic localization of sterol transcription factors Upc2p and Ecm22p in S. cerevisiae. Fungal Genet Biol 45(10):1430-8 PMID:18675371
SGD Paper PubMed Full-Text PMC

Davies BS and Rine J (2006) A role for
201 PMID:16783004
SGD Paper PubMed Full-Text PMC



Domains and Classification 7

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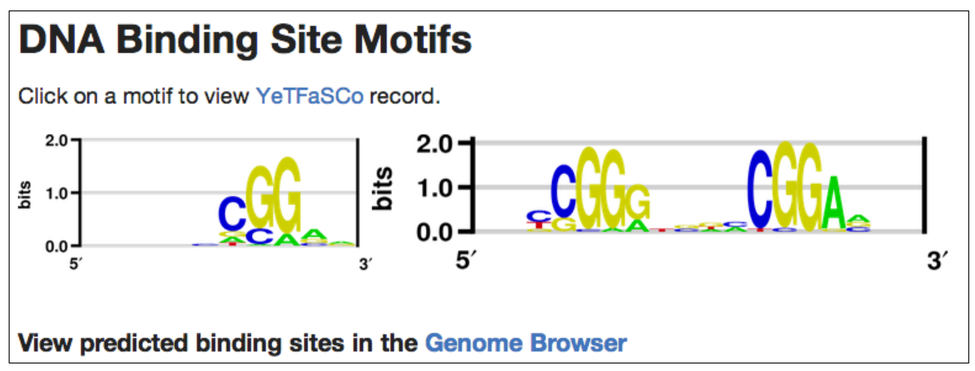
Protein Coordinates	Accession ID	Description	Source
1-814	MA0292.1	Class: Zinc-coordinating, Family: Fungal Zn cluster	JASPAR
31-85	SSF57701	Zn2/Cys6 DNA-binding domain	SUPERFAMILY
37-78	G3DSA:4.10.240.10	Zn(2)-C6 fungal-type DNA-binding domain	Gene3D
38-82	SM00066	GAL4-like Zn(II)2Cys6 (or C6 zinc) binuclear	SMART
42-80	PF00172	Zn_clus	Pfam
332-353	coil	coiled-coil	-
508-634	PF11951	Fungal_trans_2	Pfam

Showing 1 to 7 of 7 entries



Binding site motifs from the Yeast Transcription Factor Specificity Compendium (YeTFaSCo; yetfasco.ccbr.utoronto.ca)

Questions? Contact us! sgd-helpdesk@lists.stanford.edu

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